



SEQUENCE LISTING

<110> NENTSCH, Thomas J.

<120> NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
POTASSIUM CHANNELS

<130> 2815-127F

<140>

<141>

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 2335

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(2335)

<230>

<231> CDS

<232> (33)..(2170)

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cggccccagc cgggcgcgcg cc atg gcc gag gcc ccc ccg cgc cgc ctc gcc 112

Met Ala Glu Ala Pro Pro Arg Arg Leu Gly

1

5

10

ctg ggt ccc ccg ccc ggg gac gcc ccc cgc gcg gag cta gtg gcg ctc 160

Leu Gly Pro Pro Pro Gly Asp Ala Pro Arg Ala Glu Leu Val Ala Leu

15

20

25

acg gcc gtg bag agc gaa cag ggc gag gcg ggc ggg gcc gcc tcc ccg 208

Thr Ala Val Gln Ser Glu Gln Gly Glu Ala Gly Gly Gly Gly Ser Pro

30

35

40

cgc cgc ctc gcc ctc ctg gcc agc ccc ctg ccg ccg gcc gcg ccc ctc 256

Arg Arg Leu Gly Leu Leu Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu

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<p> ccc gga aac gaa ttc aac tgg ggt ttc ggt ttc ggt cag cgg tcc tgg Pro Gly Pro Gly Ser Gly Ser Gly Ser Ala Cys Gly Gln Arg Ser Ser 60 65 70 </p>	314
<p> gcc ggg cac aag cgc tac cgc cgc ctg cag aac tgg gtc tac aac gtg Ala Ala His Lys Arg Tyr Arg Arg Leu Gln Asn Trp Val Tyr Asn Val 75 80 85 90 </p>	352
<p> ctg gag cgg ccc cgc ggc tgg gcc ttc gtc tac cac gtc ttc ata ttt Leu Glu Arg Pro Arg Gly Trp Ala Phe Val Tyr His Val Phe Ile Phe 95 100 105 </p>	400
<p> ttg ctg gtc ttc agc tgc ctg gtg ctg tct gtg ctg tcc act atc cag Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Leu Ser Thr Ile Gln 110 115 120 </p>	448
<p> gag cac cag gaa ctt gcc aac gag tgt ctc ctc atc ttg gaa ttc gtg Glu His Gln Glu Leu Ala Asn Glu Cys Leu Leu Ile Leu Glu Phe Val 125 130 135 </p>	496
<p> atg atc gtg gtt ttc gcc ttg gag tac atc gtc cgg gtc tgg tcc gcc Met Ile Val Val Phe Gly Leu Glu Tyr Ile Val Arg Val Trp Ser Ala 140 145 150 </p>	544
<p> gga tgc tgc tgc cgc tac cga gga tgg cag ggt cgc ttc cgc ttt gcc Gly Cys Cys Cys Arg Tyr Arg Gly Trp Gln Gly Arg Phe Arg Phe Ala 155 160 165 170 </p>	592
<p> aga aag ccc ttc tgt gtc atc cag ttc atc gtg ttc gtg gcc tgg gtg Arg Lys Pro Phe Cys Val Ile Asp Phe Ile Val Phe Val Ala Ser Val 175 180 185 </p>	640
<p> gcc gtc atc gcc ggc ggt acc cag gcc aac atc ttc gcc acg tcc gcg Ala Val Ile Ala Ala Gly Thr Gln Gly Asn Ile Phe Ala Thr Ser Ala 190 195 200 </p>	688
<p> ctg cgc agc atg cgc ttc ctg cag atc ctg cgc atg gtg cgc atg gac Leu Arg Ser Met Arg Phe Leu Gln Ile Leu Arg Met Val Arg Met Asp 205 210 215 </p>	736
<p> cgc cgc ggc ggc acc tgg aag ctg ctg gcc tca gtg gtc tac gcg cat Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val Val Tyr Ala His 220 225 230 </p>	784
<p> agc aag gag ctg atc acc gcc tgg tac atc ggg ttc ctg gtg ctc atc Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile 235 240 245 250 </p>	832

ttc ggc ttc ttc ttc ggc gtc tac ttc ggc gag aac gac ggc aac ttc gac	976
Phe Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Asp Ala Asn Ser Asp	
255 260 265	
ttc ttc ttc tac ggc gac tgc ctc tgg tgg ggg aag att aca ttg aca	928
Phe Ser Ser Tyr Ala Asp Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr	
270 275 280	
acc atc ggc tat ggt gac aag aca ccg cac aca tgg ctg ggc agg gtc	976
Thr Ile Gly Tyr Gly Asp Lys Thr Pro His Thr Trp Leu Gly Arg Val	
285 290 295	
ctg gct gct ggc ttc ggc tta ctg ggc atc tct ttc ttt ggc ctg cct	1024
Leu Ala Ala Gly Phe Ala Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro	
300 305 310	
gcc ggc atc cta ggc ttc ggc ttt ggc ctg aag gtc cag gag cag cac	1072
Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val Gln Glu Gln His	
315 320 325 330	
cgg cag aag cac ttc gag aag cgg agg atg ccg gca gcc aac ctc atc	1120
Arg Gln Lys His Phe Glu Lys Arg Arg Met Pro Ala Ala Asn Leu Ile	
335 340 345	
cag gct gcc tgg cgc ctg tac ttc acc gat atg agc cgg gcc tac ctg	1168
Gln Ala Ala Trp Arg Leu Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu	
350 355 360	
aca gcc acc tgg tac tac tat gac agt atc ctc cca ttc ttc aga gag	1216
Thr Ala Thr Trp Tyr Tyr Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu	
365 370 375	
ctg gcc ctc ttg ttt gag cac gtg caa cgg gcc cgc aat ggg ggc cta	1264
Leu Ala Leu Leu Phe Glu His Val Gln Arg Ala Arg Asn Gly Gly Leu	
380 385 390	
cgg ccc ctg gag gtg cgg cgg ggc ccg gta ccc gac gga gca ccc tcc	1312
Arg Pro Leu Glu Val Arg Arg Ala Pro Val Pro Asp Gly Ala Pro Ser	
395 400 405 410	
cgt tac ccg ccc gtt gcc acc tgc cac cgg ccg ggc agc acc ttc ttc	1360
Arg Tyr Pro Pro Val Ala Thr Cys His Arg Pro Gly Ser Thr Ser Phe	
415 420 425	
tgc cct ggg gaa agc agc cgg atg ggc atc aaa gac cgc atc cgc atg	1408
Cys Pro Gly Glu Ser Ser Arg Met Gly Ile Lys Asp Arg Ile Arg Met	
430 435 440	

att aat ttt atg ttt ttt aat agt att ttt aat ttt ttt ttt ttt	1486
Gly Ser Ser Gln Arg Arg Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro	
445 450 455	
cca aca atg cca acc tcc cca agc agc gag cag gtg ggt gag gcc acc	1504
Pro Thr Met Pro Thr Ser Pro Ser Ser Glu Gln Val Gly Glu Ala Thr	
460 465 470	
agc ccc acc aag gtg caa aag agc tgg agc ttc aat gac cgc acc cgc	1552
Ser Pro Thr Lys Val Gln Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg	
475 480 485 490	
ttc cgg gca ttt ctg aga ctc aaa ccc cgc acc tct gct gag gat gcc	1600
Phe Arg Ala Ser Leu Arg Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala	
495 500 505	
ccc tca gag gaa gta gca gag gag aag agc tac cag tgt gag ctc acg	1648
Pro Ser Glu Glu Val Ala Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr	
510 515 520	
gtg gac gac atc atg cct gct gtg aag aca gtc atc cgc tcc atc agg	1696
Val Asp Asp Ile Met Pro Ala Val Lys Thr Val Ile Arg Ser Ile Arg	
525 530 535	
att ctc aag ttc ctg gtg gcc aaa agg aaa ttc aag gag aca ctg cga	1744
Ile Leu Lys Phe Leu Val Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg	
540 545 550	
cgg tac gac gtg aag gac gtc att gag cag tac tca gca gcc cac ctg	1792
Pro Tyr Asp Val Lys Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu	
555 560 565 570	
gac atg ctg gcc cgg atc aag agc ctg caa act cgg gtg gac caa att	1840
Asp Met Leu Gly Arg Ile Lys Ser Leu Gln Thr Arg Val Asp Gln Ile	
575 580 585	
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Val Gly Arg Gly Pro Gly Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys	
590 595 600	
ggg ccc tcc gac gcg gag gtg gtg gat gaa atc agc atg atg gga cgc	1936
Gly Pro Ser Asp Ala Glu Val Val Asp Glu Ile Ser Met Met Gly Arg	
605 610 615	
gtg gtc aag gtg gag aag cag gtg cag tcc atc gag cac aag ctg gac	1984
Val Val Lys Val Glu Lys Gln Val Gln Ser Ile Glu His Lys Leu Asp	
620 625 630	

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164	167	181	187
Arg Gly Trp Ala Gly Arg Phe Arg Phe Ala Arg Lys Pro Phe Cys Val			
	168	170	178
Ile Asp Phe Ile Val Phe Val Ala Ser Val Ala Val Ile Ala Ala Gly			
	180	185	190
Thr Gln Gly Asn Ile Phe Ala Thr Ser Ala Leu Arg Ser Met Arg Phe			
	195	200	205
Leu Gln Ile Leu Arg Met Val Arg Met Asp Arg Arg Gly Gly Thr Trp			
	210	215	220
Lys Leu Leu Gly Ser Val Val Tyr Ala His Ser Lys Glu Leu Ile Thr			
	225	230	235
Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile Phe Ala Ser Phe Leu Val			
	245	250	255
Tyr Leu Ala Glu Lys Asp Ala Asn Ser Asp Phe Ser Ser Tyr Ala Asp			
	260	265	270
Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp			
	275	280	285
Lys Thr Pro His Thr Trp Leu Gly Arg Val Leu Ala Ala Gly Phe Ala			
	290	295	300
Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser			
	305	310	315
Gly Phe Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His Phe Glu			
	325	330	335
Lys Arg Arg Met Pro Ala Ala Asn Leu Ile Gln Ala Ala Trp Arg Leu			
	340	345	350
Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu Thr Ala Thr Trp Tyr Tyr			
	355	360	365
Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu Leu Ala Leu Leu Phe Glu			
	370	375	380
His Val Gln Arg Ala Arg Asn Gly Gly Leu Arg Pro Leu Glu Val Arg			
	385	390	395
Arg Ala Pro Val Pro Asp Gly Ala Pro Ser Arg Tyr Pro Pro Val Ala			
	405	410	415
Thr Cys His Arg Pro Gly Ser Thr Ser Phe Cys Pro Gly Glu Ser Ser			
	420	425	430
Arg Met Gly Ile Lys Asp Arg Ile Arg Met Gly Ser Ser Gln Arg Arg			
	435	440	445
Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro Pro Thr Met Pro Thr Ser			
	450	455	460
Pro Ser Ser Glu Gln Val Gly Glu Ala Thr Ser Pro Thr Lys Val Gln			
	465	470	475
Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg Phe Arg Ala Ser Leu Arg			
	485	490	495
Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala Pro Ser Glu Glu Val Ala			
	500	505	510
Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr Val Asp Asp Ile Met Pro			
	515	520	525
Ala Val Lys Thr Val Ile Arg Ser Ile Arg Ile Leu Lys Phe Leu Val			

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Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys Asp		
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Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Gly Arg Ile		560
	565	570
Lys Ser Leu Gln Thr Arg Val Asp Gln Ile Val Gly Arg Gly Pro Gly		575
	580	585
Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys Gly Pro Ser Asp Ala Glu		590
	595	600
Val Val Asp Glu Ile Ser Met Met Gly Arg Val Val Lys Val Glu Lys		605
	610	615
Gln Val Gln Ser Ile Glu His Lys Leu Asp Leu Leu Leu Gly Phe Tyr		620
	625	630
Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala Ser Leu Gly Ala Val Gln		635
	645	650
Val Pro Leu Phe Asp Pro Asp Ile Thr Ser Asp Tyr His Ser Pro Val		655
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Asp His Glu Asp Ile Ser Val Ser Ala Gln Thr Leu Ser Ile Ser Arg		670
	675	680
Ser Val Ser Thr Asn Met Asp		685
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<10> 3
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 <12> DNA
 <13> Artificial Sequence

<20>
 <23> Description of Artificial Sequence: PCR Primer

<40> 3
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24

<10> 4
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 <13> Artificial Sequence

<20>
 <23> Description of Artificial Sequence: PCR Primer

<40> 4
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24

<211> 6
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<220>
<220> Description of Artificial Sequence: PCR Primer

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23

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<220>
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<212> DNA
<213> Artificial Sequence

<220>
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<211> 8
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<212> DNA
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<220>
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<110> 10
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<220>
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21

<110> 11
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<220>
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21

<110> 12
<111> 21
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

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21

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<11> Artificial Sequence

<120>
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21

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<113> Artificial Sequence

<120>
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<110> 15
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<120>
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<220>
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<400> 17
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<210> 18
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<220>
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<400> 18
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<400> 19
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<400> 20
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<210> 21
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<210> 23
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<220>
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<220>
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<223> Description of Artificial Sequence: PCR Primer

<400> 17
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<211> 23

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

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<210> 31

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<223> Description of Artificial Sequence: PCR Primer

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<210> 32

<211> 24

<212> DNA

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<223> Description of Artificial Sequence: PCR Primer

<400> 32

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24

<211> 187
 <212> 187
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<400> 33

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Trp Gly Arg Leu Pro Gly Ala Arg Arg Gly Ser Ala Gly Leu Ala Lys
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Lys Cys Pro Phe Ser Leu Glu Leu Ala Glu Gly Gly Pro Ala Gly Gly
 35 40 45

Ala Leu Tyr Ala Pro Ile Ala Pro Gly Ala Pro Gly Pro Ala Pro Pro
 50 55 60

Ala Ser Pro Ala Ala Pro Ala Ala Pro Pro Val Ala Ser Asp Leu Gly
 65 70 75 80

Pro Arg Pro Pro Val Ser Leu Asp Pro Arg Val Ser Ile Tyr Ser Thr
 85 90 95

Arg Arg Pro Val Leu Ala Arg Thr His Val Gln Gly Arg Val Tyr Asn
 100 105 110

Phe Leu Glu Arg Pro Thr Gly Trp Lys Cys Phe Val Tyr His Phe Ala
 115 120 125

Val Phe Leu Ile Val Leu Val Cys Leu Ile Phe Ser Val Leu Ser Thr
 130 135 140

Ile Glu Gln Tyr Ala Ala Leu Ala Thr Gly Thr Leu Phe Trp Met Glu
 145 150 155 160

Ile Val Leu Val Val Phe Phe Gly Thr Glu Tyr Val Val Arg Leu Trp
 165 170 175

Ser Ala Gly Cys Arg Ser Lys Tyr Val Gly Leu Trp Gly Arg Leu Arg
 180 185 190

Phe Ala Arg Lys Pro Ile Ser Ile Ile Asp Leu Ile Val Val Val Ala
 195 200 205

Ser Met Val Val Leu Cys Val Gly Ser Lys Gly Gln Val Phe Ala Thr
 210 215 220

Ser Ala Ile Arg Gly Ile Arg Ile Leu Gln Ile Leu Arg Met Leu His
 225 230 235 240

Val Asp Arg Gln Gly Gly Thr Trp Arg Leu Leu Gly Ser Val Val Phe
 245 250 255

Ile His Arg Gln Glu Leu Ile Thr Thr Leu Tyr Ile Gly Phe Leu Gly
 260 265 270

Leu Ile Phe Ser Ser Tyr Phe Val Tyr Leu Ala Gln Lys Asp Ala Val
 275 280 285

Asn Glu Ser Gly Arg Val Glu Phe Gly Ser Tyr Ala Asp Ala Leu Trp
 290 295 300

Trp Gly Val Val Thr Val Thr Thr Ile Gly Tyr Gly Asp Lys Val Pro
 305 310 315 320

Gln Thr Trp Val Gly Lys Thr Ile Ala Ser Cys Phe Ser Val Phe Ala
 325 330 335

Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala
 340 345 350

Leu Lys Val Gln Gln Lys Gln Arg Gln Lys His Phe Asn Arg Gln Ile
 355 360 365

Pro Ala Ala Ala Ser Leu Ile Gln Thr Ala Trp Arg Cys Tyr Ala Ala
 370 375 380

Glu Asn Pro Asp Ser Ser Thr Trp Lys Ile Tyr Ile Arg Lys Ala Pro
 385 390 395 400

Arg Ser His Thr Leu Leu Ser Pro Ser Pro Lys Pro Lys Lys Ser Val
 405 410 415

Val Val Lys Lys Lys Lys Phe Lys Leu Asp Lys Asp Asn Gly Val Thr
 420 425 430

Pro Gly Glu Lys Met Leu Thr Val Pro His Ile Thr Cys Asp Pro Pro
 435 440 445

Glu Glu Arg Arg Leu Asp His Phe Ser Val Asp Gly Tyr Asp Ser Ser
 450 455 460

Val Arg Lys Ser Pro Thr Leu Leu Glu Val Ser Met Pro His Phe Met
 465 470 475 480

Arg Thr Asn Ser Ile Ala His Asp Leu Asp Leu Gln Gly Gln Thr Leu
485 490 495

Leu Thr Pro Ile Thr His Ile Ser Gln Leu Arg Gln His His Arg Ala
500 505 510

Thr Ile Lys Val Ile Arg Arg Met Gln Tyr Phe Val Ala Lys Lys Lys
515 520 525

Phe Gln Gln Ala Arg Lys Pro Tyr Asp Val Arg Asp Val Ile Gln Gln
530 535 540

Tyr Ser Gln Gly His Leu Asn Leu Met Val Arg Ile Lys Glu Leu Gln
545 550 555 560

Arg Arg Leu Asp Gln Ser Ile Gly Lys Pro Ser Leu Phe Ile Ser Val
565 570 575

Ser Glu Lys Ser Lys Asp Arg Gly Ser Asn Thr Ile Gly Ala Arg Leu
580 585 590

Asn Arg Val Glu Asp Lys Val Thr Gln Leu Asp Gln Arg Leu Ala Leu
595 600 605

Ile Thr Asp Met Leu His Gln Leu Leu Ser Leu His Gly Gly Ser Thr
610 615 620

Pro Gly Ser Gly Gly Pro Pro Arg Glu Gly Gly Ala His Ile Thr Gln
625 630 635 640

Pro Cys Gly Ser Gly Gly Ser Val Asp Pro Glu Leu Phe Leu Pro Ser
645 650 655

Asn Thr Leu Pro Thr Tyr Glu Gln Leu Thr Val Pro Arg Arg Gly Pro
660 665 670

Asp Glu Gly Ser
675

(210) 34

(211) 844

(212) PRT

(213) Homo sapiens

(400) 34

Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly

1

5

10

15

Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
20 30 40 50

Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
35 40 45

Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
50 55 60

Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
65 70 75 80

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
85 90 95

Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
100 105 110

Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
115 120 125

Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
130 135 140

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
145 150 155 160

Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
165 170 175

Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
210 215 220

Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
225 230 235 240

Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
245 250 255

Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
260 265 270

Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
 275 280 285

Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
 290 295 300

Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
 305 310 315 320

Gln Gln Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
 325 330 335

Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
 340 345 350

Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
 355 360 365

Val Pro Met Tyr Arg Leu Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu
 370 375 380

Arg Asn Leu Lys Ser Lys Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro
 385 390 395 400

Pro Glu Pro Ser Pro Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe
 405 410 415

Ser Ser Pro Arg Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala
 420 425 430

Gln Thr Val Arg Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser
 435 440 445

Pro Ser Lys Val Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala
 450 455 460

Arg Gln Ala Phe Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu
 465 470 475 480

Glu Ala Ser Leu Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro
 485 490 495

Cys Glu Phe Val Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile
 500 505 510

Arg Ala Val Cys Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys
 515 520 525

Val Ser Leu Arg Pro Tyr Asp Val Met Asp Val Ile Glu Gln Tyr Ser
 530 535 540

Ala Gly His Leu Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg
 545 550 555 560

Val Asp Gln Ile Val Gly Arg Gly Pro Ala Ile Thr Asp Lys Asp Arg
 565 570 575

Thr Lys Gly Pro Ala Glu Ala Glu Leu Pro Glu Asp Pro Ser Met Met
 580 585 590

Gly Arg Leu Gly Lys Val Glu Lys Gln Val Leu Ser Met Glu Lys Lys
 595 600 605

Leu Asp Phe Leu Val Asn Ile Tyr Met Gln Arg Met Gly Ile Pro Pro
 610 615 620

Thr Glu Thr Glu Ala Tyr Phe Gly Ala Lys Glu Pro Glu Pro Ala Pro
 625 630 635 640

Pro Tyr His Ser Pro Glu Asp Ser Arg Glu His Val Asp Arg His Gly
 645 650 655

Cys Ile Val Lys Ile Val Arg Ser Ser Ser Ser Thr Gly Gln Lys Asn
 660 665 670

Phe Ser Ala Pro Pro Ala Ala Pro Pro Val Gln Cys Pro Pro Ser Thr
 675 680 685

Ser Trp Gln Pro Gln Ser His Pro Arg Gln Gly His Gly Thr Ser Pro
 690 695 700

Val Gly Asp His Gly Ser Leu Val Arg Ile Pro Pro Pro Pro Ala His
 705 710 715 720

Glu Arg Ser Leu Ser Ala Tyr Gly Gly Gly Asn Arg Ala Ser Met Glu
 725 730 735

Phe Leu Arg Gln Glu Asp Thr Pro Gly Cys Arg Pro Pro Glu Gly Thr
 740 745 750

Leu Arg Asp Ser Asp Thr Ser Ile Ser Ile Pro Ser Val Asp His Glu
 755 760 765

Glu Leu Glu Arg Ser Phe Ser Gly Phe Ser Ile Ser Gln Ser Lys Glu
 770 775 780

Asn Leu Asp Ala Leu Asn Ser Cys Tyr Ala Ala Val Ala Pro Cys Ala
 785 790 795 800

Lys Val Arg Pro Tyr Ile Ala Glu Gly Glu Ser Asp Thr Asp Ser Asp
 805 810 815

Leu Cys Thr Pro Cys Gly Pro Pro Pro Arg Ser Ala Thr Gly Glu Gly
 820 825 830

Pro Phe Gly Asp Val Gly Trp Ala Gly Pro Arg Lys
 835 840

(210) 35

(211) 872

(212) PRT

(213) Homo sapiens

(400) 35

Met Gly Leu Lys Ala Arg Arg Ala Ala Gly Ala Ala Gly Gly Gly Gly
 1 5 10 15

Asp Gly Gly Gly Gly Gly Gly Gly Ala Ala Asn Pro Ala Gly Gly Asp
 20 25 30

Ala Ala Ala Ala Gly Asp Glu Glu Arg Lys Val Gly Leu Ala Pro Gly
 35 40 45

Asp Val Glu Gln Val Thr Leu Ala Leu Gly Ala Gly Ala Asp Lys Asp
 50 55 60

Gly Thr Leu Leu Leu Glu Gly Gly Gly Arg Asp Glu Gly Gln Arg Arg
 65 70 75 80

Thr Pro Gln Gly Ile Gly Leu Leu Ala Lys Thr Pro Leu Ser Arg Pro
 85 90 95

Val Lys Arg Asn Asn Ala Lys Tyr Arg Arg Ile Gln Thr Leu Ile Tyr
 100 105 110

Asp Ala Leu Glu Arg Pro Arg Gly Trp Ala Leu Leu Tyr His Ala Leu
 115 120 125

Val Phe Leu Ile Val Leu Gly Cys Leu Ile Leu Ala Val Leu Thr Thr
 130 135 140

Phe Lys Gln Tyr Gln Thr Val Ser Gly Asp Trp Leu Leu Leu Leu Glu

161		166		169
Thr Phe Ala Ile Phe Ile Phe Gly Ala Glu Phe Ala Leu Arg Ile Trp				
	165	170		175
Ala Ala Gly Cys Cys Cys Arg Tyr Lys Gly Trp Arg Gly Arg Leu Lys				
	180	185		190
Phe Ala Arg Lys Pro Leu Cys Met Leu Asp Ile Phe Val Leu Ile Ala				
	195	200		205
Ser Val Pro Val Val Ala Val Gly Asn Gln Gly Asn Val Leu Ala Thr				
	210	215		220
Ser Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met Leu Arg Met				
	225	230		235
Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Ala Ile Cys Ala				
	245	250		255
His Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Thr Leu				
	260	265		270
Ile Leu Ser Ser Phe Leu Val Tyr Leu Val Glu Lys Asp Val Pro Glu				
	275	280		285
Val Asp Ala Gln Gly Glu Glu Met Lys Glu Glu Phe Glu Thr Tyr Ala				
	290	295		300
Asp Ala Leu Trp Trp Gly Leu Ile Thr Leu Ala Thr Ile Gly Tyr Gly				
	305	310		315
Asp Lys Thr Pro Lys Thr Trp Glu Gly Arg Leu Ile Ala Ala Thr Phe				
	325	330		335
Ser Leu Ile Gly Val Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly				
	340	345		350
Ser Gly Leu Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His Phe				
	355	360		365
Glu Lys Arg Arg Lys Pro Ala Ala Glu Leu Ile Gln Ala Ala Trp Arg				
	370	375		380
Tyr Tyr Ala Thr Asn Pro Asn Arg Ile Asp Leu Val Ala Thr Trp Arg				
	385	390		395
Phe Tyr Glu Ser Val Val Ser Phe Pro Phe Phe Arg Lys Glu Gln Leu				
				400

418 419 420
 Ala Ala Ala Ser Ser Gln Lys Leu Gly Leu Leu Asp Arg Val Arg Leu
 421 425 430
 Ser Asn Pro Arg Gly Ser Asn Thr Lys Gly Lys Leu Phe Thr Pro Leu
 435 440 445
 Asn Val Asp Ala Ile Glu Glu Ser Pro Ser Lys Glu Pro Lys Pro Val
 450 455 460
 Gly Leu Asn Asn Lys Glu Arg Phe Arg Thr Ala Phe Arg Met Lys Ala
 465 470 475 480
 Tyr Ala Phe Trp Gln Ser Ser Glu Asp Ala Gly Thr Gly Asp Pro Met
 485 490 495
 Ala Glu Asp Arg Gly Tyr Gly Asn Asp Phe Pro Ile Glu Asp Met Ile
 500 505 510
 Pro Thr Leu Lys Ala Ala Ile Arg Ala Val Arg Ile Leu Gln Phe Arg
 515 520 525
 Leu Tyr Lys Lys Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys
 530 535 540
 Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Ser Arg
 545 550 555 560
 Ile Lys Tyr Leu Gln Thr Arg Ile Asp Met Ile Phe Thr Pro Gly Pro
 565 570 575
 Pro Ser Thr Pro Lys His Lys Lys Ser Gln Lys Gly Ser Ala Phe Thr
 580 585 590
 Phe Pro Ser Gln Gln Ser Pro Arg Asn Glu Pro Tyr Val Ala Arg Pro
 595 600 605
 Ser Thr Ser Glu Ile Glu Asp Gln Ser Met Met Gly Lys Phe Val Lys
 610 615 620
 Val Glu Arg Gln Val Gln Asp Met Gly Lys Lys Leu Asp Phe Leu Val
 625 630 635 640
 Asp Met His Met Gln His Met Glu Arg Leu Gln Val Gln Val Thr Glu
 645 650 655
 Tyr Tyr Pro Thr Lys Gly Thr Ser Ser Pro Ala Glu Ala Glu Lys Lys

Ala Asp Asn Arg Tyr Ser Asp Leu Lys Thr Ile Ile Cys Asn Tyr Ser
675 680 685

Glu Thr Gly Pro Pro Glu Pro Pro Tyr Ser Phe His Gln Val Thr Ile
690 695 700

Asp Lys Val Ser Pro Tyr Gly Phe Phe Ala His Asp Pro Val Asn Leu
705 710 715 720

Pro Arg Gly Gly Pro Ser Ser Gly Lys Val Gln Ala Thr Pro Pro Ser
725 730 735

Ser Ala Thr Thr Tyr Val Glu Arg Pro Thr Val Leu Pro Ile Leu Thr
740 745 750

Leu Leu Asp Ser Arg Val Ser Cys His Ser Gln Ala Asp Leu Gln Gly
755 760 765

Pro Tyr Ser Asp Arg Ile Ser Pro Arg Gln Arg Arg Ser Ile Thr Arg
770 775 780

Asp Ser Asp Thr Pro Leu Ser Leu Met Ser Val Asn His Glu Glu Leu
785 790 795 800

Glu Arg Ser Pro Ser Gly Phe Ser Ile Ser Gln Asp Arg Asp Asp Tyr
805 810 815

Val Phe Gly Pro Asn Gly Gly Ser Ser Trp Met Arg Glu Lys Arg Tyr
820 825 830

Leu Ala Glu Gly Glu Thr Asp Thr Asp Thr Asp Pro Phe Thr Pro Ser
835 840 845

Gly Ser Met Pro Leu Ser Ser Thr Gly Asp Gly Ile Ser Asp Ser Val
850 855 860

Trp Thr Pro Ser Asn Lys Pro Ile
865 870

<210> 36

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<210> Description of Artificial Sequence: PCR Primer

<400> 36

aaggctggat cagtcattg g

21

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 37

agggggcag gctgttgctg g

21

<210> 38

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 38

ggcagcac ctccccctg g

21

<210> 39

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 39

ctctatgcaa tgtagggct gac

23

<210> 40

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<210> Description of Artificial Sequence: PCR Primer

<400> 4

aaagaaatc aacatatagt agc

24

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: PCR Primer

<400> 41

cagaagagtc aagatgggca ggac

24